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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Wed Apr 12 07:46:37 2000; MasPar time 36.61 Seconds
 Tabular output not generated.

Title: >US-09-276-268-16
 Description: (1-338) from US09276268.pep
 Perfect Score: 2401
 Sequence: 1 MGAVWSALLVGGGLAGALI.....NREFLQTHEDKVVHGWGWIH 338

Scoring table: PAM 150
 Gap 11

Searched: 225878 seqs., 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: sptrnbl12

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phage 10:sp_plant 11:sp_rabbit 12:sp_undclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 47.028; Variance 99.789; scale 0.471

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.	Medline
1	1381	57.5	358	4	095210 GENETHONIN 1.	2.14e-238	RA BOUJOT S., LIGNON M.-F., PIETU G., LE CUNFF M., LEGER J.-J., RA AUFFRAY C., DECHESNE C.A.; RT "Molecular cloning and functional expression of a novel human gene, GENETHONIN 1. Encoding two 41-43 kDa skeletal muscle internal membrane proteins." RL Biochem. J. 335:549-556(1998).
2	163	6.8	579	3	022596 GLUCOAMYLASE G2 (EC 3.2.1.37e-04	1.28e-08	DR EMBL; AF062534; AAC788271; -.
3	135	5.6	613	2	059222 ALPHA-AMYLASE (EC 3.2.1.89e-04	1.37e-04	RA MARIAGE-SAMPSON R., HOUIGATE R., SOULARUE P., AUFFRAY C.; RT Novel gene transcripts preferentially expressed in human muscles revealed by quantitative hybridization of a high density cDNA array." RL Genome Res. 6:492-503(1996). [2]
4	134	5.6	1378	5	097405 COLLAGEN PRO ALPHA-CHA MINI-COLLAGEN PRECURSOR	1.89e-04	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
5	128	5.3	149	5	004848 F9D12.19 PROTEIN.	1.24e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
6	128	5.3	491	10	081504 F57B.3 PROTEIN.	1.24e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
7	124	5.2	295	5	020927 GLUCOAMYLASE.	4.23e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
8	125	5.2	638	3	022296 BETA-AMYLASE (EC 3.2.1.91e-02	3.12e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
9	123	5.1	546	2	0924N9 PRECOLLAGEN P PRECURSO	5.74e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
10	123	5.1	902	5	016161 PRECOLLAGEN P PRECURSO	5.74e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
11	122	5.1	1366	6	046392 TYPE I PROCOLLAGEN PRO	7.77e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
12	122	5.1	1453	11	063079 COLLAGEN ALPHA1 (PROAGM	7.77e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
13	122	5.1	1460	6	0XJS77 TYPE I COLLAGEN PRO-AL	7.77e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
14	125	5.1	1461	4	076045 PRO ALPHA 1(I) COLLAGEN	7.77e-03	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
15	120	5.0	150	6	0XJT24 TYPE II COLLAGEN CYANO	1.42e-02	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
16	119	5.0	290	5	F58F6.2 PROTEIN.	1.91e-02	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
17	119	5.0	347	6	Q9XT25 TYPE II COLLAGEN CYANO	1.91e-02	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
18	119	5.0	684	5	P06079 FIBRILLAR COLLAGEN (FR	1.91e-02	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
19	119	5.0	692	2	CYCLODEXTRIN GLYCOSYL	1.91e-02	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;
20	120	5.0	853	2	PGRS-FAMILY PROTEIN.	1.42e-02	RA SEQUENCE 358 AA; 39007 MW; BBCS12D6 CRC32;

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	358 AA.
ID	095210			
AC	095210;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DE	GENETHONIN 1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE= MUSCLE;			
RX	MEDLINE; 96425596.			
RA	PIETU G., ALIBERT O., GUICHARD V., LAMY B., BOIS F., LEROU E., MARIAGE-SAMPSON R., HOUIGATE R., SOULARUE P., AUFFRAY C.; RT Novel gene transcripts preferentially expressed in human muscles revealed by quantitative hybridization of a high density cDNA array." RL Genome Res. 6:492-503(1996). [2]			
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	RESULT	Y113I30 standard; Protein; 56 AA.
y	22	MASLJCGPKLAACGIVLSANGVIMLMLGIFFNVHAYLIEDVPFIEKDFENGPNQIYN 81
b	61	LYEQVSYNCFIAGLYLLGGSFSCVRLNRKEYAVR 98
y	82	LYEQVSYNCFIAGLYLLGGSFSCVRLNRKEYAVR 119

Query Match 66.2%; Score 1575; DB 1; Length 263;
 Best Local Similarity 79.4%; Pred. No. 6.11e-155;
 Matches 201; Conservative 27; Mismatches 23; Indels 2; Gaps 2;

Db 6 PGPLWLPAGALAWAVGFVSS-MGSGNPAPGCIVWLQGQEATCSLVLIQDTDTRAECAS 64
 Qy 3 SGALWPLMGLWVTVGSAYNGSEDSPGGCIVWLQGREATCSLVLKTRVSRECCAS 62

Db 65 GNIDTAWSNLTHPGNKNILLGFLGLVRLCPKDSCDGVECGPKACRMGGPR-CIECAP 123
 Qy 63 GINNTAASNFTHPGNKNSLLGFLGLVCLPCKDSCDGVECGPKACRNAGGASNNCBEVP 122

Db 124 DCSCLPARIQVCSGDATYRDCELRAARCRGHDLSYMRGRCRKSCEHVCPRPOSVC 183
 Qy 123 NCGGFPAGFQVCGSDGATYRDCELRAARCRHDPDLYMRCRCSQAQVYCPRPQSL 182

Db 184 VDGTGSAHCIVVYRAACPVPVSSPGQELCGNNNNTYISSCHMRQATCPLGRSTGVRHAGC 243
 Qy 183 VDGTGSAHCIVVYRAACPVPVSPGQELCGNNNNTYISSCHLRQATCPLGRSTGVRHAGC 242

Db 244 AGTPEEPGGSEA 256
 Qy 243 TGGPKFLKSGDAA 255

RESULT 2
 ID R74600 standard; Protein: 319 AA.
 AC R74600;
 DT 24-OCT-1995 (first entry)
 DE Folllistatin.
 KW Neuronal differentiation; transforming growth factor; TGF-beta;
 degenerative disorders; nervous system; Alzheimer's disease;
 Parkinson's disease; amyotrophic lateral disease; Pick's disease;
 Huntington's disease; multiple sclerosis; anoxia-ischaemia; trauma;
 ageing; tachycardia; atrial cardiac arrhythmia.
 KW Synthetic.
 OS WO9510611.
 PD 20-APR-1995.
 PF 14-OCT-1995; 117450.
 PR 14-OCT-1993; US-136748.
 PA (HARD) Harvard College.
 PI Melton D, Hemmati-Brivanlou A;
 DR WPI; 95-178527/23.
 N-PDBB; Q90017.

PT Inducing neuronal differentiation using TGF-beta family agonist -
 PT useful to prevent death and/or degeneration of neuronal cells, e.g.
 PT to treat Alzheimer's disease, multiple sclerosis, etc.
 PS Example: Page 41; 53pp; English.

CC The sequence is that of follistatin. This protein can be used to
 differentiate neuronal cell phenotype by antagonizing the action of
 at least one member of the transforming growth factor beta (TGF-beta)
 family which normally induces the cell to differentiate to a non-
 neuronal phenotype. The agent can be used to prevent death and/or
 degeneration of a neuronal cell in a degenerative disorder of the
 nervous system, e.g. 9. Alzheimer's disease, Parkinson's disease,
 amyotrophic lateral sclerosis, Pick's disease, Huntington's disease,
 multiple sclerosis, neuronal damage resulting from anoxia-ischaemia
 or trauma and neuronal degeneration associated with ageing.

SQ Sequence 319 AA;

Query Match 33.5%; Score 796; DB 1; Length 319;
 Best Local Similarity 46.0%; Pred. No. 1.22e-70;
 Matches 99; Conservative 46; Mismatches 67; Indels 3; Gaps 3;

Db 26 AVQAGNCWILQOSKNGRCVQVLVRTELSKECCCTGRJLGSWTEEDVPNSTLFPKWMIFHGGAA 85
 Qy 30 SVPGGYCIVWLQGREATCSVLKTRVSRECCASGNINTAASNFTHGNKI-SLGLFLGLV 88

Db 86 PHCIPCKETCENVDGPGKCKMKKKNNPKRCVYCAPDCSNITWKGSVGDGKTYDECAL 145
 Qy 89 -HCLPCDKDSGIVCGSPKACRNAGGASNNCEVPRCEGFPAGFVCGSDGATYRDEC 147

Db 146 LKAICKGVPPEDVQYQGCKKTCRDVLCPGSSSCVYDTONNAYCUTCNRI-CPEPTSPDQ 204
 Qy 148 RTARCRGHDDLRWYRGRCQSKCAQVIVCPRPOSCLVDTGSAHCIVVCRAAFCPVPSNPGQ 207

Db 205 YLCGNDGITYGACHLRKATCLGRSIGLAYEGKC 239
 Qy 208 ELCGNNNTYISSCHLRQATCFLGRSIGVRHAGC 242

RESULT 3
 ID P93396 standard; protein: 317 AA.
 AC P93396;
 DT 15-JUL-1990 (first entry)
 DE Human follistatin precursor protein as encoded by cDNA
 KW Human follistatin precursor protein; signal sequence;
 testicular lambda gt11 cDNA library; porcine follistatin precursor.
 OS Homo sapiens.
 PH Key
 FT misc_difference 4 .5
 FT misc_difference 4 .5
 /note="In pfs this is PK"
 FT misc_difference 163
 /note="In pfs this is K"
 FT misc_difference 200
 /note="In pfs this is T"
 FT misc_difference 276
 /note="In pfs this is E"
 FT misc_difference 280
 /note="In pfs this is E"
 FT region 124
 /note="potential N-linked glycosylation site"
 FT region 258
 /note="potential N-linked glycosylation site"
 FT peptide 1 .29
 /note="signal peptide"
 FT protein 30 .317
 PN WO8901945-A.
 PD 09-MAR-1989.
 PF 26-AUG-1988; WO2971.
 PR 26-JUL-1988; US-224432.
 PS (SALK) Salk Inst for Biol Stud.
 PI Ling NCK, Ueno N, Shimasaki S, Ying SY, Guillemain RCL;
 CC A testicular lambda gt11 cDNA library was screened with a cDNA probe
 CC encoding the first 317 amino acids of the porcine F5 (pfs) precursor.
 CC 12 positive clones were obtained. From the nucleotide sequences of
 CC the clones, it was determined that there is encoded an hFS precursor
 CC containing a 344 amino acid sequence which is highly homologous with
 CC the 344 residue pfs precursor. It differs from the 344 residue pfs
 CC precursor by only 6 residues (see FT). p93396 is encoded by bases 28-978
 CC of n90611. 317 AA;

Query Match 33.2%; Score 789; DB 1; Length 317;
 Best Local Similarity 45.6%; Pred. No. 6.31e-70;
 Matches 99; Conservative 46; Mismatches 69; Indels 3; Gaps 3;

Db 24 DRSQAGNCWILQOSKNGRCVQVLVRTELSKECCCTGRJLGSWTEEDVPNSTLFPKWMIFHGGAA 83
 Qy 28 EDSYVPGGYCIVWLQGREATCSVLKTRVSRECCASNNINTAASNFTHGNKI-SLGLFLGLV 86

Db 84 GAPNCIPCKETCENVDGPGKCKMKKKNNPKRCVYCAPDCSNITWKGSVGDGKTYRDEC 143
 Qy 87 LV-HCLPCDKDSGIVCGSPKACRNAGGASNNCEVPRCEGFPAGFVCGSDGATYRDEC 145

Db 144 ALLKARCKEOPPELEQYQGCKKTCRDVLCPGSSSCVYDTONNAYCUTCNRI-CPEPASS 202
 Qy 146 ELRTARCRGHDDLRWYRGRCQSKCAQVIVCPRPOSCLVDTGSAHCIVVCRAAFCPVPSNPGQ 205

Best Local Similarity 79.4%; Pred. No. 1.03e-13;
 Matches 20; Conservative 27; Mismatches 23; Indels 2; Gaps 2;

Matches 66; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

6 PGPLWPLPGALAWANGFVSS-MGSGSNPAPGCVNLIQGOEATCSLYLQTDYTRAECCAS 64
 3 SGALWPLNGALVYTFYGSVCAVMGSDVSQGCVNLIQGREATCSLYLKTYSRECCAS 62

65 GNIDIAWSNLTHPGKINLIGFLGLIVCPCDKDSCDGVECGPKACRMLGGPR-CECAP 123
 63 GNINTAWSNTHPGKISLIGFLGLVHCLPKCDKSDGVECGPKACRNAGGASNCECVP 122

124 DCSSIPARLQVCGSGDAGTYDECELRARCRGHPDLSVATGRCRKSCSEHVCPRPOS CV 183
 123 NCEGFPAFGVCGSGDAGTYDECELRARCRGHPDLSVATGRCRKSCAQVVCPRQSCL 182

184 VDQTGSABCVCRAPCPVPSGPGBELGCGNNVITYISSCHMRQATCFGLRSIGTVRHAGSC 243
 183 VDQTSAHCVCRAPCPVPSNPQGELCGNNVITYISSCHLRAQFCFLGRSIGVRHGPIC 242

244 AGTPEPEPGGESA 256
 243 TGGPKFLKGDA 255

RESULT 2
 US-08-972-008-5 STANDARD; PRT; 73 AA.

Sequence 5, Application US/08972008

Sequence 5, Application US/08972008
 Patent No. 5942420

GENERAL INFORMATION:
 APPLICANT: Holtzman, Douglas A.
 TITLE OF INVENTION: No. 5942420el Molecules of the Follistatin-Related
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/972,008
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandrigoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: MNI-026
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 73 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: Internal
 SEQUENCE 73 AA: 7674 MW; 26282 CN;

Match Similarity 21.8%; Score 519; DB 2; Length 73;
 real Similarity 90.4%; Pred. No. 1.1e-38;

Matches 1 CEHYCPRPOSQYDGTGSAHCVVCRAPCPVPSGPQELCGNNVITYISSCHMRQATCF 60
 QY 170 CAQVCPRPOSQYDGTGSAHCVVCRAPCPVPSNPQELCGNNVITYISSCHMRQATCF 229

Db 61 LGRSIGYRHAGSC 73
 QY 230 LGRSIGYRHGPIC 242

RESULT 3
 ID 5225348-1 STANDARD; PRT; 501 AA.
 XX
 AC *****
 XX
 XX DT 01-JAN-1900

Patent No. 5225348
 CC APPLICANT: HAGATA, SHIGEKAZU; SUGANO, SUMIO; KIM, DONG W.;
 CC UETSUKI, TAICHI; KAITO, YOSHITO
 CC TITLE OF INVENTION: DNA FRAGMENT AND EXPRESSION PLASMID
 CC CONTAINING THE DNA FRAGMENT
 CC NUMBER OF SEQUENCES: 9
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/447,823
 CC SEQ ID NO:1:
 CC LENGTH: 08-DEC-1989
 SQ SEQUENCE 501 AA; 54436 MW; 1431850 CN;

Query Match 21.4%; Score 510; DB 4; Length 462;
 Best Local Similarity 79.0%; Pred. No. 1.06e-37;
 Matches 79; Conservative 5; Mismatches 13; Indels 3; Gaps 3;

Db 363 CHTAHIAKFAELKEKIDRSRGKLEDDPKFLKGDAIVDAYPGKPMCVESFSDYPPLG 422
 QY 221 CHLROATC-FLGRSIGV RHPGIC-TGGPKFLKGDAIVDAYPGKPMCVESFSDYPLG 277

Db 423 REAVRDHQTVAYGVIRAKDVKKAAGAGKVTSQAQKAK 462
 QY 278 REAVRDHQTVAYGVIRAKDVKKAAGAGKVTSQAQKAK 317

RESULT 4
 ID US-08-371-377-18 STANDARD; PRT; 462 AA.
 XX
 AC *****
 XX
 DT

Sequence 18, Application US/08371377

Sequence 18, Application US/08371377
 CC Patent No. 5851164
 CC GENERAL INFORMATION:
 CC APPLICANT: Fisher, Paul B.
 CC ADDRESS: Shenzhen, Shenzhen, China
 CC TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND
 CC IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EX-
 CC MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
 CC NUMBER OF SEQUENCES: 22
 CC CORRESPONDENCE ADDRESS:
 CC STREET: 1185 Avenue of the Americas
 CC CITY: New York
 CC STATE: New York
 CC COUNTRY: United States of America
 CC ZIP: 10016

Computer readable form:
 Medium type: Floppy disk
 Computer: IBM PC compatible
 Operating system: PC-DOS/MS-DOS
 Software: PatentIn Release #1.0, Version #1.25
 Current application data:
 Application number: US/08/972,008
 Filing date:
 Classification: 435
 Attorney/agent information:
 Name: Amy E. Mandrigoras
 Registration number: 36,207
 Reference/docket number: MNI-026
 Telecommunication information:
 Telephone: (617)227-7400
 Telex: (617)742-4214
 Information for seq id no: 5:
 Sequence characteristics:
 Length: 73 amino acids
 Type: amino acid
 Topology: linear
 Molecule type: Peptide
 Fragment type: Internal
 Sequence 73 AA: 7674 MW; 26282 CN;